

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/162,597DATE: 01/06/99
TIME: 20:33:28

INPUT SET: S30604.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Bandman, Olga
Au-Young, Janice
Goli, Surya K.
Hillman, Jennifer.
Zweiger, Gary B.

(ii) TITLE OF THE INVENTION: A NOVEL TUMOR PROTEIN

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: U.S.
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/162,597
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/715,204
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0126 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

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47
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 204 amino acids
50 (B) TYPE: amino acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
53
54 (ii) MOLECULE TYPE: peptide
55 (vii) IMMEDIATE SOURCE:
56 (A) LIBRARY:
57 (B) CLONE: Consensus
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 Met Glu Ala Gln Ala Gln Gly Leu Leu Glu Thr Glu Pro Leu Gln Gly
62 1 5 10 15
63 Thr Asp Glu Asp Ala Val Ala Ser Ala Asp Phe Ser Ser Met Leu Ser
64 20 25 30
65 Glu Glu Glu Lys Glu Glu Leu Lys Ala Glu Leu Val Gln Leu Glu Asp
66 35 40 45
67 Glu Ile Thr Thr Leu Arg Gln Val Leu Ser Ala Lys Glu Arg His Leu
68 50 55 60
69 Val Glu Ile Lys Gln Lys Leu Gly Met Asn Leu Met Asn Glu Leu Lys
70 65 70 75 80
71 Gln Asn Phe Ser Lys Ser Trp His Asp Met Gln Thr Thr Thr Ala Tyr
72 85 90 95
73 Lys Lys Thr His Glu Thr Leu Ser His Ala Gly Gln Lys Ala Thr Ala
74 100 105 110
75 Ala Phe Ser Asn Val Gly Thr Ala Ile Ser Lys Lys Phe Gly Asp Met
76 115 120 125
77 Ser Tyr Ser Ile Arg His Ser Ile Ser Met Pro Ala Met Arg Asn Ser
78 130 135 140
79 Pro Thr Phe Lys Ser Phe Glu Glu Arg Val Glu Thr Thr Val Thr Ser
80 145 150 155 160
81 Leu Lys Thr Lys Val Gly Gly Thr Asn Pro Asn Gly Gly Ser Phe Glu
82 165 170 175
83 Glu Val Leu Ser Ser Thr Ala His Ala Ser Ala Gln Ser Leu Ala Gly
84 180 185 190
85 Gly Ser Arg Arg Thr Lys Glu Glu Glu Leu Gln Cys
86 195 200
87

88 (2) INFORMATION FOR SEQ ID NO:2:
89

90 (i) SEQUENCE CHARACTERISTICS:
91 (A) LENGTH: 790 base pairs
92 (B) TYPE: nucleic acid
93 (C) STRANDEDNESS: single
94 (D) TOPOLOGY: linear
95
96 (ii) MOLECULE TYPE: cDNA
97
98 (vii) IMMEDIATE SOURCE:
99 (A) LIBRARY:

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(B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

104	GGGCCAGCTG	CGTTCTGAGC	CTGGGCGCAG	CTACCATCTG	CTCTGGGAAG	CACCAGGGTG	60
105	TCCCCGCCGC	CCTCAGCTCG	AAGTCAGCCA	CCATGGAGGC	GCAGGCACAA	GGTTTGTGG	120
106	AGACTGAACC	GTTGCAAGGA	ACAGACGAAG	ATGCAGTAGC	CAGTGCTGAC	TTCTCTAGCA	180
107	TGCTCTCTGA	GGAGGAAAAG	GAAGAGTTAA	AAGCAGAGTT	AGTTCAGCTA	GAAGACGAAA	240
108	TTACAACACT	ACGACAAGTT	TTGTCAGCGA	AAGAAAAGGCA	TCTAGTTGAG	ATAAAACAAA	300
109	AACTCGGCAT	GAACCTGATG	AATGAATTAA	AACAGAACTT	CAGCAAAAGC	TGGCATGACA	360
110	TGCAGACTAC	CACTGCCTAC	AAGAAAACAC	ATGAAACCCT	GAGTCACGCA	GGGCAAAAGG	420
111	CAACTGCAGC	TTTCAGCAAC	GTTGGAACGG	CCATCAGCAA	GAAGTTCGGA	GACATGAGTT	480
112	ACTCCATTGC	CCATTCCATA	AGTATGCCTG	CTATGAGGAA	TTCTCCTACT	TTCAAATCAT	540
113	TTGAGGAGAG	GGTTGAGACA	ACTGTCACAA	GCCTCAAGAC	GAAAGTAGGC	GGTACGAACC	600
114	CTAATGGAGG	CAGTTTTGAG	GAGGTCTCA	GCTCCACGGC	CCATGCCAGT	GCCCAGAGCT	660
115	TGGCAGGAGG	CTCCCGGCGG	ACCAAGGAGG	AGGAGCTGCA	GTGCTAAGTC	CAGCCAGCGT	720
116	GCAGTGCATC	CAGAAACCGG	CCACTACCCA	GCCCATCTNT	GCCTGTGCTT	ATCCAGATAA	780
117	GAAGACCAAA						790

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

135	Met	Thr	Leu	Phe	His	Phe	Gly	Asn	Cys	Phe	Ala	Leu	Ala	Tyr	Phe	Pro
136	1				5					10					15	
137	Tyr	Phe	Ile	Thr	Tyr	Lys	Cys	Ser	Gly	Leu	Ser	Glu	Tyr	Asn	Ala	Phe
138				20					25					30		
139	Trp	Lys	Cys	Val	Gln	Ala	Gly	Val	Thr	Tyr	Leu	Phe	Val	Gln	Leu	Cys
140			35				40						45			
141	Lys	Met	Leu	Phe	Leu	Ala	Thr	Phe	Phe	Pro	Thr	Trp	Glu	Gly	Gly	Ile
142		50					55					60				
143	Tyr	Asp	Phe	Ile	Gly	Glu	Phe	Met	Lys	Ala	Ser	Val	Asp	Val	Ala	Asp
144	65				70					75					80	
145	Leu	Ile	Gly	Leu	Asn	Leu	Val	Met	Ser	Arg	Asn	Ala	Gly	Lys	Gly	Glu
146				85					90					95		
147	Tyr	Lys	Ile	Met	Val	Ala	Ala	Leu	Gly	Trp	Ala	Thr	Ala	Glu	Leu	Ile
148				100					105					110		
149	Met	Ser	Arg	Cys	Ile	Pro	Leu	Trp	Val	Gly	Ala	Arg	Gly	Ile	Glu	Phe
150			115					120					125			
151	Asp	Trp	Lys	Tyr	Ile	Gln	Met	Ser	Ile	Asp	Ser	Asn	Ile	Ser	Leu	Val
152			130				135					140				

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153  His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp
154  145                               150                               155                               160
155  Leu Tyr His Asn Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser
156                               165                               170                               175
157  Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu
158                               180                               185                               190
159  Gly Ser Trp Ala Arg Leu Asp Ala Arg Ala Val Val Thr Gly Leu Leu
160                               195                               200                               205
161  Ala Leu Lys His Phe Gly Pro Val Cys Arg Arg Cys Gln Cys Ala Leu
162                               210                               215                               220
163  Leu Gly Leu Val Ser Gln Thr Leu Met Tyr Leu Phe Pro Ala Ser Leu
164  225                               230                               235                               240
165  Gln Val Leu Val Lys
166                               245
167

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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184  GTMGMKCGCG GGCCCCCGCC AGTCAGGTGG GTGCCAGGCC CTGGCCGTGG CGAAAGAGCC      60
185  GGCGGAGGGA GGACCCGCTC CCGGAGACGC CGCCTCGCGA TCCCCGCGCG GGCGGGACCG      120
186  GGCGGCCGCG ATCATGACCC TGTTTCACTT CGGGAAGTGC TTCGCTCTTG CCTACTTCCC      180
187  CTACTTCATC ACCTACAAGT GCAGCGGCCT GTCCGAGTAC AACGCCTTCT GGAAATGCGT      240
188  CCAGGCTGGA GTCACCTACC TCTTTGTCCA ACTCTGCAAG ATGCTGTTCT TGGCCACTTT      300
189  CTTTCCCACC TGGGAAGGCG GCATCTATGA CTTCATTGGG GAGTTCATGA AGGCCAGCGT      360
190  GGATGTGGCA GACCTGATAG GTCTAAACCT TGTCATGTCC CGGAATGCCG GCAAGGGAGA      420
191  GTACAAGATC ATGGTTGCTG CCCTGGGCTG GGCCACTGCT GAGCTTATTA TGTCCCGCTG      480
192  CATTCCCCTA TGGGTCGGAG CCCGGGGCAT TGAGTTTGAC TGGAAGTACA TCCAGATGAG      540
193  CATAGACTCC AACATCAGTC TGGTCCATTA CATCGTCGCG TCTGCTCAGG TCTGGATGAT      600
194  AACACGCTAT GATCTGTACC ACAACTTCCG GCCAGCTGTC CTTCTGCTGA TGTTCCCTCAG      660
195  TGTCTACAAG GCCTTTGTTA TGGAGACCTT CGTCCACCTC TGCTCGCTGG GCAGTTGGGC      720
196  ARCTCTAMTG GCCCCGAGCAG TGGTAACGGG GCTGCTGGCC CTCAAGCACT TTGGSCCTGT      780
197  ATGTCGSCGT TGTCATGTG CACTYCTAGG CTTGGTGTCT CAGACATTGA TGTACCTTTT      840
198  CCCTGCCTCA CTCCAGGTTT TAGTGAAGTA AACAGTATTT GGAAAGTT      888
199

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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206 (D) TOPOLOGY: linear
207
208 (ii) MOLECULE TYPE: peptide
209
210 (vii) IMMEDIATE SOURCE:
211 (A) LIBRARY: GenBank
212 (B) CLONE: 790225
213
214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
215
216 Met Asp Arg Gly Glu Gln Gly Leu Leu Arg Thr Asp Pro Val Pro Glu
217 1 5 10 15
218 Glu Gly Glu Asp Val Ala Ala Thr Ile Ser Ala Thr Glu Thr Leu Ser
219 20 25 30
220 Glu Glu Glu Gln Glu Glu Leu Arg Arg Glu Leu Ala Lys Val Glu Glu
221 35 40 45
222 Glu Ile Gln Thr Leu Ser Gln Val Leu Ala Ala Lys Glu Lys His Leu
223 50 55 60
224 Ala Glu Ile Lys Arg Lys Leu Gly Ile Asn Ser Leu Gln Glu Leu Lys
225 65 70 75 80
226 Gln Asn Ile Ala Lys Gly Trp Gln Asp Val Thr Ala Thr Ser Ala Tyr
227 85 90 95
228 Lys Lys Thr Ser Glu Thr Leu Ser Gln Ala Gly Gln Lys Ala Ser Ala
229 100 105 110
230 Ala Phe Ser Ser Val Gly Ser Val Ile Thr Lys Lys Leu Glu Asp Val
231 115 120 125
232 Lys Asn Ser Pro Thr Phe Lys Ser Phe Glu Glu Lys Val Glu Asn Leu
233 130 135 140
234 Lys Ser Lys Val Gly Gly Thr Lys Pro Ala Gly Gly Asp Phe Gly Glu
235 145 150 155 160
236 Val Leu Asn Ser Ala Ala Asn Ala Ser Ala Thr Thr Thr Glu Pro Leu
237 165 170 175
238 Pro Glu Lys Thr Gln Glu Ser Leu
239 180
240
241 (2) INFORMATION FOR SEQ ID NO:6:
242
243 (i) SEQUENCE CHARACTERISTICS:
244 (A) LENGTH: 257 amino acids
245 (B) TYPE: amino acid
246 (C) STRANDEDNESS: single
247 (D) TOPOLOGY: linear
248
249 (ii) MOLECULE TYPE: peptide
250
251 (vii) IMMEDIATE SOURCE:
252 (A) LIBRARY: GenBank
253 (B) CLONE: 1072344
254
255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
256
257 Met Pro Lys Gly Asn Lys Lys Pro Asn Glu Lys Lys Glu Glu Leu Glu
258 1 5 10 15

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text